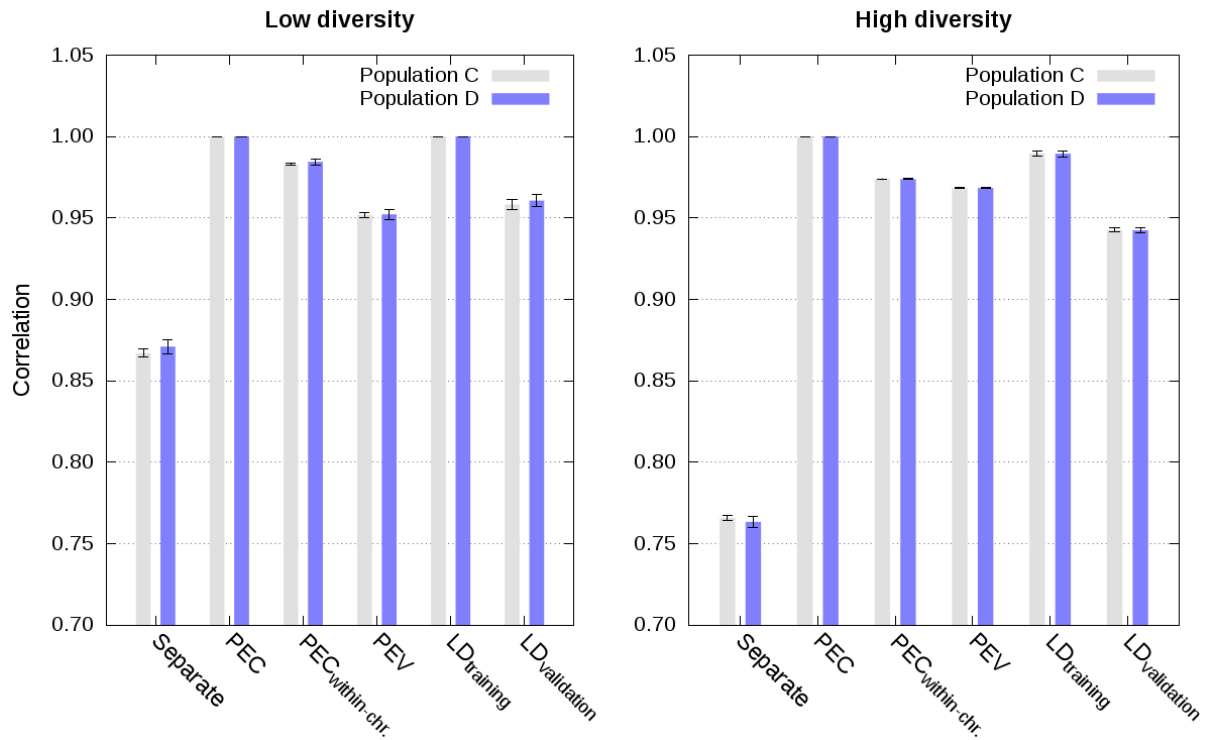
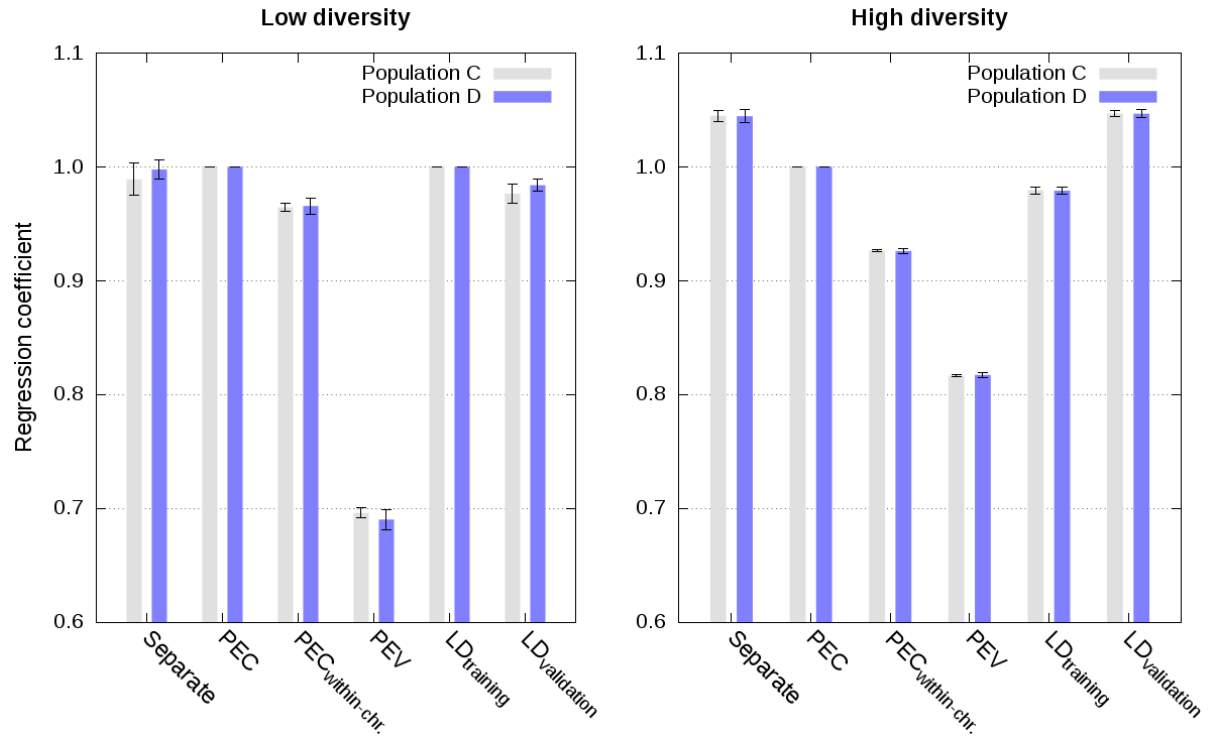


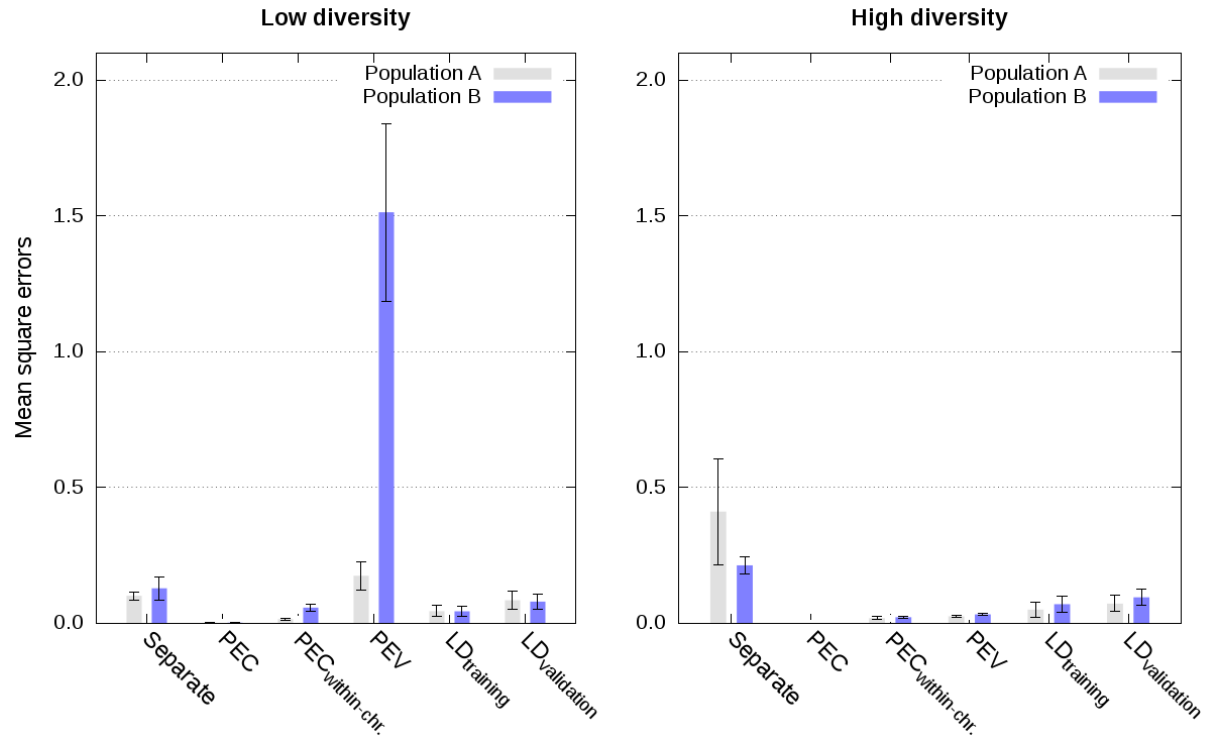
## SUPPLEMENTAL FIGURES



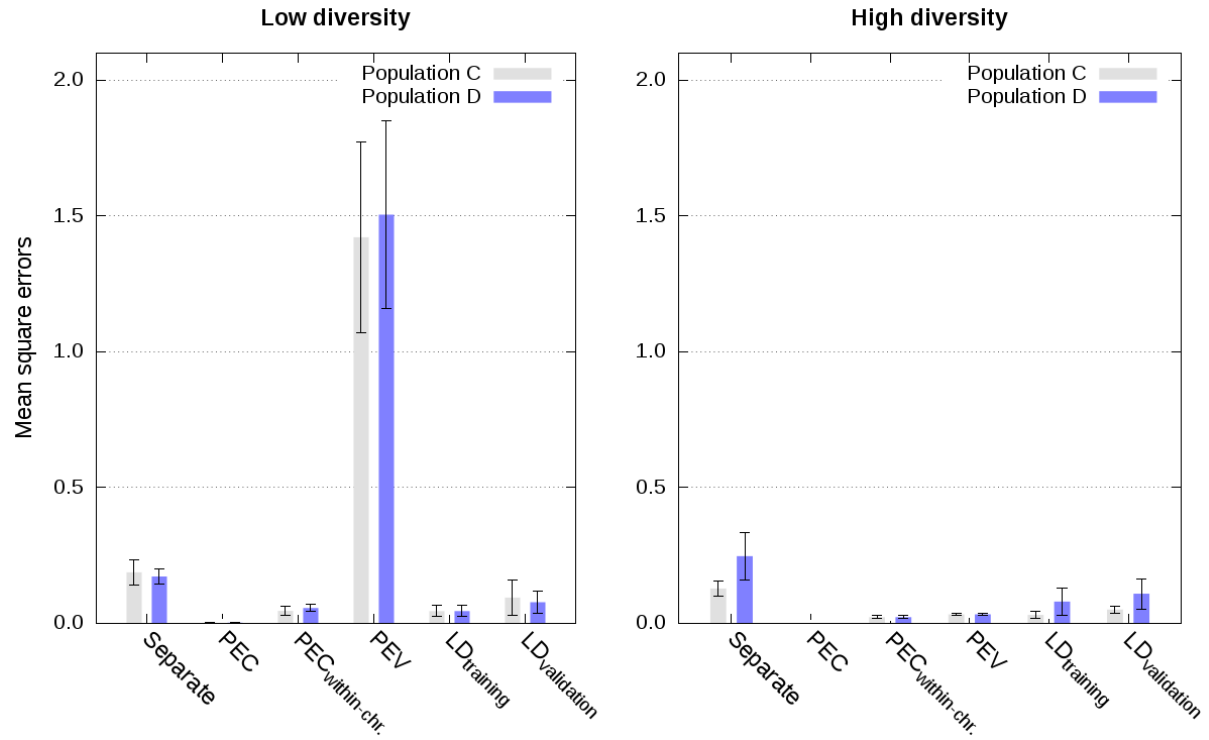
**Figure S1 - Correlation between estimated genetic values from the joint analysis and from different analyses in populations C and D using a single phenotype record per individual in scenarios with low and high diversity (values are averages across the five replicates with standard errors).**



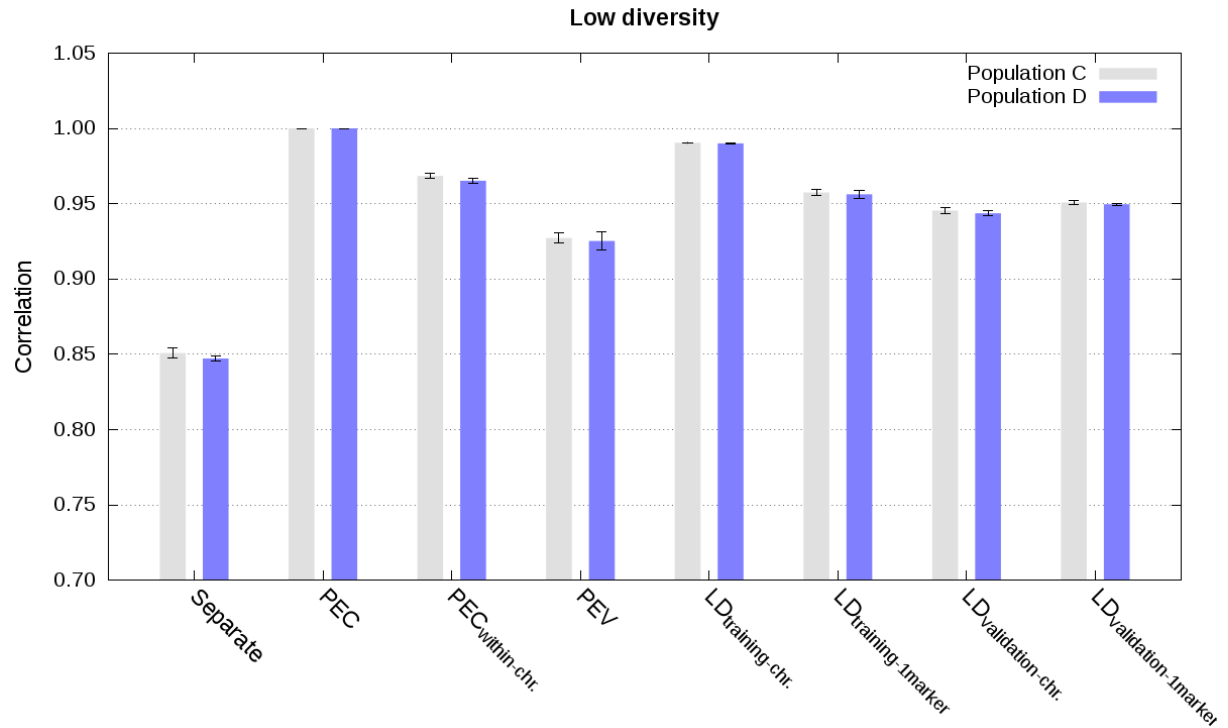
**Figure S2 – Regression of estimated genetic values from the joint analysis on estimated genetic values from different analyses in populations C and D using a single phenotype record per individual in scenarios with low and high diversity (values are averages across the five replicates with standard errors).**



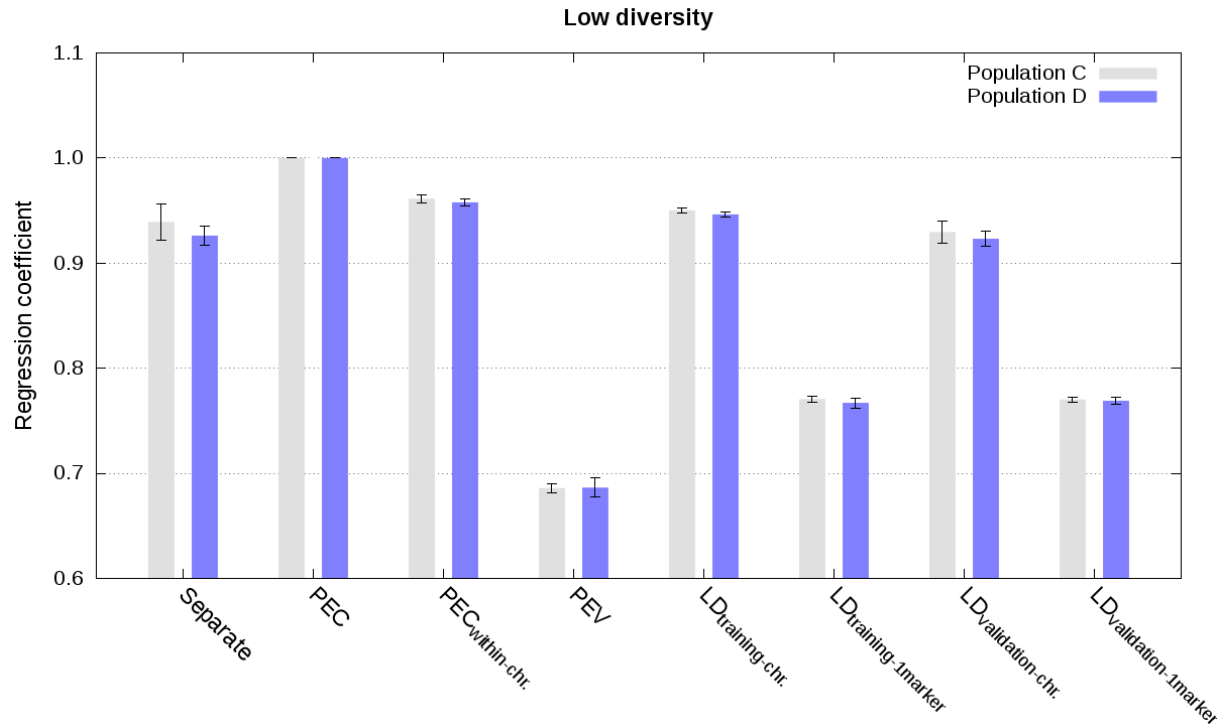
**Figure S3 - Mean square errors between joint estimated genetic values from the joint analysis and from different analyses in populations A and B using a single phenotype record per individual in scenarios with low and high diversity (values are averages across the five replicates with standard errors).**



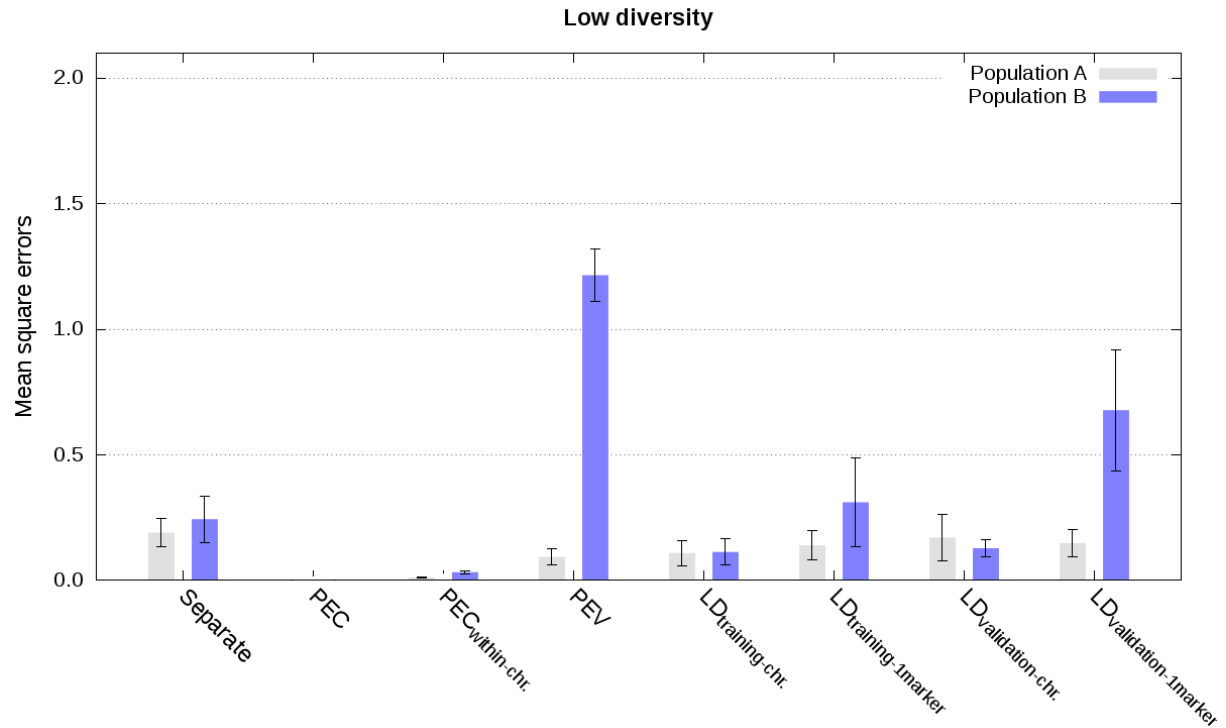
**Figure S4 - Mean square errors between joint estimated genetic values from the joint analysis and from different analyses in populations C and D using a single phenotype record per individual in scenarios with low and high diversity (values are averages across the five replicates with standard errors).**



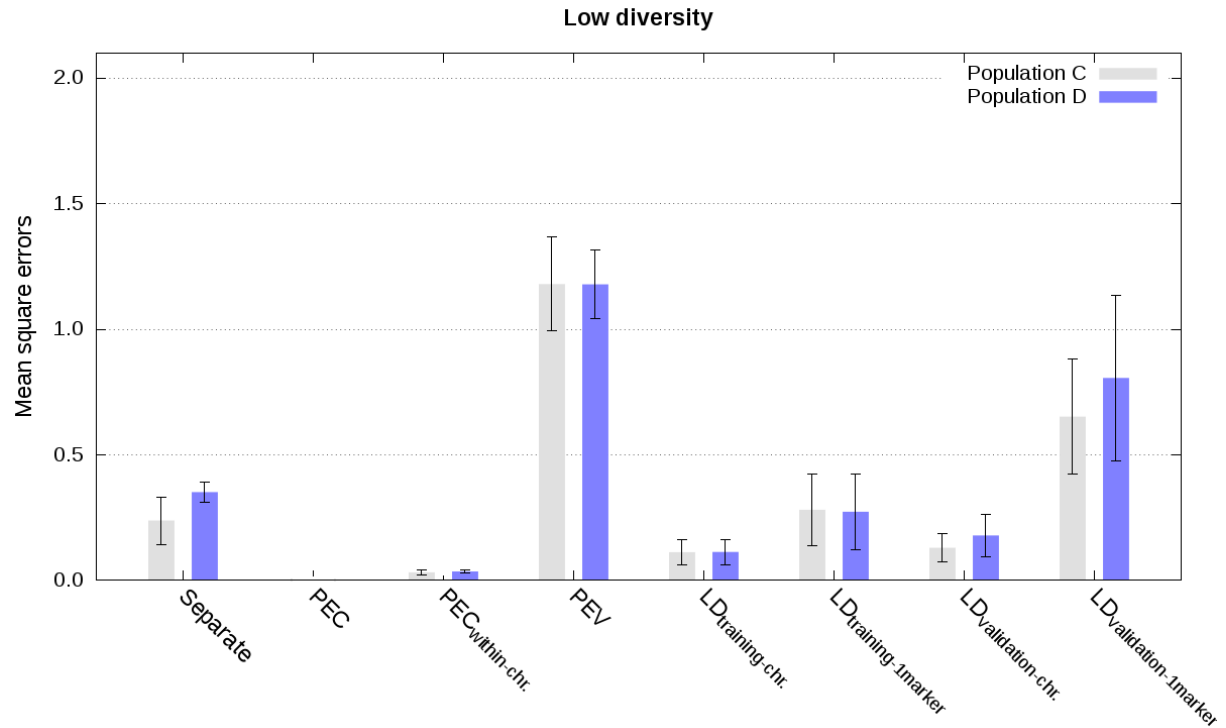
**Figure S5 - Correlation between estimated genetic values from the joint analysis and from different analyses in populations C and D using weighted phenotype records in the scenario with low diversity (values are averages across the five replicates with standard errors).**



**Figure S6 - Regression of estimated genetic values from the joint analysis on estimated genetic values from different analyses in populations C and D using weighted phenotype records in the scenario with low diversity (values are averages across the five replicates with standard errors).**



**Figure S7 - Mean square errors between estimated genetic values from the joint analysis and from different analyses in populations A and B using weighted phenotype records in the scenario with low diversity (values are averages across the five replicates with standard errors).**



**Figure S8 - Mean square errors between estimated genetic values from the joint analysis and from different analyses in populations C and D using weighted phenotype records in the scenario with low diversity (values are averages across the five replicates with standard errors).**